Hiroyuki Kurata

List of Publications by Year
in descending order

85	2,010	236612 25	276539 41
papers	citations	h-index	g-index

91	91	91	1443
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of a reliable sacral-sparing examination to assess the ASIA impairment scale in patients with traumatic spinal cord injury. Journal of Spinal Cord Medicine, 2024, 47, 286-292.	0.7	0
2	Recent Development of Bioinformatics Tools for microRNA Target Prediction. Current Medicinal Chemistry, 2022, 29, 865-880.	1.2	9
3	BERT6mA: prediction of DNA N6-methyladenine site using deep learning-based approaches. Briefings in Bioinformatics, 2022, 23, .	3.2	23
4	Deepm5C: A deep-learning-based hybrid framework for identifying human RNA N5-methylcytosine sites using a stacking strategy. Molecular Therapy, 2022, 30, 2856-2867.	3.7	40
5	iACVP: markedly enhanced identification of anti-coronavirus peptides using a dataset-specific word2vec model. Briefings in Bioinformatics, 2022, 23, .	3.2	17
6	Meta-i6mA: an interspecies predictor for identifying DNAN6-methyladenine sites of plant genomes by exploiting informative features in an integrative machine-learning framework. Briefings in Bioinformatics, 2021, 22, .	3.2	86
7	Critical evaluation of web-based DNA N6-methyladenine site prediction tools. Briefings in Functional Genomics, 2021, 20, 258-272.	1.3	29
8	IRC-Fuse: improved and robust prediction of redox-sensitive cysteine by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2021, 35, 315-323.	1.3	5
9	PUP-Fuse: Prediction of Protein Pupylation Sites by Integrating Multiple Sequence Representations. International Journal of Molecular Sciences, 2021, 22, 2120.	1.8	8
10	Virtual metabolic human dynamic model for pathological analysis and therapy design for diabetes. IScience, 2021, 24, 102101.	1.9	14
11	PredNTS: Improved and Robust Prediction of Nitrotyrosine Sites by Integrating Multiple Sequence Features. International Journal of Molecular Sciences, 2021, 22, 2704.	1.8	16
12	NeuroPred-FRL: an interpretable prediction model for identifying neuropeptide using feature representation learning. Briefings in Bioinformatics, 2021, 22, .	3.2	56
13	Robust in-phase synchronization in repressor-based coupled gene oscillators. IFAC-PapersOnLine, 2021, 54, 574-579.	0.5	1
14	RCGAToolbox: A Real-coded Genetic Algorithm Software for Parameter Estimation of Kinetic Models. IPSJ Transactions on Bioinformatics, 2021, 14, 30-35.	0.2	2
15	i4mC-ROSE, a bioinformatics tool for the identification of DNA N4-methylcytosine sites in the Rosaceae genome. International Journal of Biological Macromolecules, 2020, 157, 752-758.	3.6	74
16	Coupling protocol of interlocked feedback oscillators in circadian clocks. Journal of the Royal Society Interface, 2020, 17, 20200287.	1.5	4
17	iLBE for Computational Identification of Linear B-cell Epitopes by Integrating Sequence and Evolutionary Features. Genomics, Proteomics and Bioinformatics, 2020, 18, 593-600.	3.0	30
18	ProIn-Fuse: improved and robust prediction of proinflammatory peptides by fusing of multiple feature representations. Journal of Computer-Aided Molecular Design, 2020, 34, 1229-1236.	1.3	33

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19	i6mA-Fuse: improved and robust prediction of DNA 6ÂmA sites in the Rosaceae genome by fusing multiple feature representation. Plant Molecular Biology, 2020, 103, 225-234.	2.0	59
20	i4mC-Mouse: Improved identification of DNA N4-methylcytosine sites in the mouse genome using multiple encoding schemes. Computational and Structural Biotechnology Journal, 2020, 18, 906-912.	1.9	57
21	Computer-Aided Rational Design of Efficient NADPH Production System by Escherichia coli pgi Mutant Using a Mixture of Glucose and Xylose. Frontiers in Bioengineering and Biotechnology, 2020, 8, 277.	2.0	3
22	A prediction model of functional outcome at 6 months using clinical findings of a person with traumatic spinal cord injury at 1 month after injury. Spinal Cord, 2020, 58, 1158-1165.	0.9	12
23	Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. Current Genomics, 2020, 21, 194-203.	0.7	8
24	Evolution of Sequence-based Bioinformatics Tools for Protein-protein Interaction Prediction. Current Genomics, 2020, 21, 454-463.	0.7	25
25	Efficient computational model for identification of antitubercular peptides by integrating amino acid patterns and properties. FEBS Letters, 2019, 593, 3029-3039.	1.3	38
26	Computational identification of microbial phosphorylation sites by the enhanced characteristics of sequence information. Scientific Reports, 2019, 9, 8258.	1.6	32
27	Ranking network mechanisms by how they fit diverse experiments and deciding on E. coli's ammonium transport and assimilation network. Npj Systems Biology and Applications, 2019, 5, 14.	1.4	25
28	PreAIP: Computational Prediction of Anti-inflammatory Peptides by Integrating Multiple Complementary Features. Frontiers in Genetics, 2019, 10, 129.	1.1	85
29	Large-Scale Assessment of Bioinformatics Tools for Lysine Succinylation Sites. Cells, 2019, 8, 95.	1.8	42
30	Prediction of S-nitrosylation sites by integrating support vector machines and random forest. Molecular Omics, 2019, 15, 451-458.	1.4	48
31	Self-replenishment cycles generate a threshold response. Scientific Reports, 2019, 9, 17139.	1.6	6
32	Improved kinetic model of Escherichia coli central carbon metabolism in batch and continuous cultures. Journal of Bioscience and Bioengineering, 2018, 125, 251-257.	1.1	27
33	SIPMA: A Systematic Identification of Protein-Protein Interactions in Zea mays Using Autocorrelation Features in a Machine-Learning Framework. , 2018, , .		6
34	iLMS, Computational Identification of Lysine-Malonylation Sites by Combining Multiple Sequence Features. , 2018, , .		5
35	libRCGA: a C library for real-coded genetic algorithms for rapid parameter estimation of kinetic models. IPSJ Transactions on Bioinformatics, 2018, 11, 31-40.	0.2	6
36	GPSuc: Global Prediction of Generic and Species-specific Succinylation Sites by aggregating multiple sequence features. PLoS ONE, 2018, 13, e0200283.	1.1	59

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37	A Comprehensive Review of In silico Analysis for Protein S-sulfenylation Sites. Protein and Peptide Letters, 2018, 25, 815-821.	0.4	23
38	Computational Modeling of Lysine Post-Translational Modification: An Overview. Current Synthetic and Systems Biology, 2018, 06, .	0.3	7
39	Mathematical comparison of memory functions between mutual activation and repression networks in a stochastic environment. Journal of Theoretical Biology, 2017, 427, 28-40.	0.8	5
40	Computational identification of protein S-sulfenylation sites by incorporating the multiple sequence features information. Molecular BioSystems, 2017, 13, 2545-2550.	2.9	56
41	Syntheses of Partially Brominated Derivatives of Tetra-2-thienylmethane for Three-Dimensionally Extended Ï€-Electron Systems. Heterocycles, 2017, 95, 615.	0.4	0
42	Robustness analysis of the detailed kinetic model of an ErbB signaling network by using dynamic sensitivity. PLoS ONE, 2017, 12, e0178250.	1.1	2
43	Development of an accurate kinetic model for the central carbon metabolism of Escherichia coli. Microbial Cell Factories, 2016, 15, 112.	1.9	42
44	In vitro evaluation of a combination treatment involving anticancer agents and an aurora kinase B inhibitor. Oncology Letters, 2016, 12, 4263-4269.	0.8	5
45	S-system-based analysis of the robust properties common to many biochemical network models. Bioprocess and Biosystems Engineering, 2016, 39, 735-746.	1.7	1
46	Metabolic analysis of antibody producing Chinese hamster ovary cell culture under different stresses conditions. Journal of Bioscience and Bioengineering, 2016, 122, 117-124.	1.1	5
47	Web application for genetic modification flux with database to estimate metabolicÂfluxes of genetic mutants. Journal of Bioscience and Bioengineering, 2016, 122, 111-116.	1.1	0
48	Dynamic Modeling of Metabolic and Gene Regulatory Systems toward Developing Virtual Microbes. Journal of Chemical Engineering of Japan, 2014, 47, 1-9.	0.3	4
49	CADLIVE toolbox for MATLAB: automatic dynamic modeling of biochemical networks with comprehensive system analysis. Bioprocess and Biosystems Engineering, 2014, 37, 1925-1927.	1.7	7
50	Complementary elementary modes for fast and efficient analysis of metabolic networks. Biochemical Engineering Journal, 2014, 90, 121-130.	1.8	19
51	Analytical study of robustness of a negative feedback oscillator by multiparameter sensitivity. BMC Systems Biology, 2014, 8, S1.	3.0	5
52	Flux module decomposition for parameter estimation in a multiple-feedback loop model of biochemical networks. Bioprocess and Biosystems Engineering, 2013, 36, 333-344.	1.7	8
53	Robust complementary hierarchical clustering for gene expression data analysis by Î²-divergence. Journal of Bioscience and Bioengineering, 2013, 116, 397-407.	1.1	12
54	CADLIVE optimizer: web-based parameter estimation for dynamic models. Source Code for Biology and Medicine, 2012, 7, 9.	1.7	3

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55	A Symmetric Dual Feedback System Provides a Robust and Entrainable Oscillator. PLoS ONE, 2012, 7, e30489.	1.1	11
56	Application of Approximate Pattern Matching in Two Dimensional Spaces to Grid Layout for Biochemical Network Maps. PLoS ONE, 2012, 7, e37739.	1.1	9
57	Biological Design Principles of Complex Feedback Modules in theE. coliAmmonia Assimilation System. Artificial Life, 2011, 18, 53-90.	1.0	12
58	An integrative and practical evolutionary optimization for a complex, dynamic model of biological networks. Bioprocess and Biosystems Engineering, 2011, 34, 433-446.	1.7	13
59	Quasi-multiparameter sensitivity measure for robustness analysis of complex biochemical networks. Journal of Theoretical Biology, 2011, 272, 174-186.	0.8	11
60	CADLIVE Converter for constructing a biochemical network map. Biochemical Engineering Journal, 2011, 54, 200-206.	1.8	3
61	Use of maximum entropy principle with Lagrange multipliers extends the feasibility of elementary mode analysis. Journal of Bioscience and Bioengineering, 2010, 110, 254-261.	1.1	21
62	Diffusion Model Based Spectral Clustering for Protein-Protein Interaction Networks. PLoS ONE, 2010, 5, e12623.	1.1	25
63	Alternating Covalent Bonding Interactions in a One-Dimensional Chain of a Phenalenyl-Based Singlet Biradical Molecule Having KekulÃ© Structures. Journal of the American Chemical Society, 2010, 132, 14421-14428.	6.6	162
64	Maximum entropy decomposition of flux distribution at steady state to elementary modes. Journal of Bioscience and Bioengineering, 2009, 107, 84-89.	1.1	28
65	A gradual update method for simulating the steady-state solution of stiff differential equations in metabolic circuits. Bioprocess and Biosystems Engineering, 2009, 32, 283-288.	1.7	1
66	Genetic modification of flux for flux prediction of mutants. Bioinformatics, 2009, 25, 1702-1708.	1.8	18
67	Two-phase Search (TPS) Method: Nonbiased and High-speed Parameter Search for Dynamic Models of Biochemical Networks. IPSJ Transactions on Bioinformatics, 2009, 2, 2-14.	0.2	9
68	Visualizing Global Properties of Large Complex Networks. PLoS ONE, 2008, 3, e2541.	1.1	4
69	Extended CADLIVE: a novel graphical notation for design of biochemical network maps and computational pathway analysis. Nucleic Acids Research, 2007, 35, e134-e134.	6.5	31
70	Mathematical Identification of Critical Reactions in the Interlocked Feedback Model. PLoS ONE, 2007, 2, e1103.	1.1	16
71	Integration of enzyme activities into metabolic flux distributions by elementary mode analysis. BMC Systems Biology, 2007, 1, 31.	3.0	39
72	Module-Based Analysis of Robustness Tradeoffs in the Heat Shock Response System. PLoS Computational Biology, 2006, 2, e59.	1.5	89

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73	A grid layout algorithm for automatic drawing of biochemical networks. Bioinformatics, 2005, 21, 2036-2042.	1.8	57
74	CADLIVE dynamic simulator: Direct link of biochemical networks to dynamic models. Genome Research, 2005, 15, 590-600.	2.4	56
75	CADLIVE for constructing a large-scale biochemical network based on a simulation-directed notation and its application to yeast cell cycle. Nucleic Acids Research, 2003, 31, 4071-4084.	6.5	69
76	Screening for transgenic plant cells that highly express a target gene from genetically mixed cells. Biochemical Engineering Journal, 2002, 10, 175-182.	1.8	5
77	Intermittent light irradiation with second- or hour-scale periods controls anthocyanin production by strawberry cellsâ˜†. Enzyme and Microbial Technology, 2000, 26, 621-629.	1.6	29
78	Mathematical model analyzes light-controlled expression of the CHS promoter in BY-2 cells. Biochemical Engineering Journal, 1999, 4, 65-72.	1.8	2
79	Software of Living Systems.. Kagaku Kogaku Ronbunshu, 1999, 25, 169-176.	0.1	0
80	Title is missing!. Biotechnology Letters, 1998, 20, 463-468.	1.1	3
81	The light/dark cycle operation with an hour-scale period enhances caffeine production by Coffea arabica cells. Enzyme and Microbial Technology, 1998, 23, 518-523.	1.6	11
82	Light irradiation causes physiological and metabolic changes for purine alkaloid production by a Coffea arabica cell suspension culture. Plant Science, 1997, 123, 197-203.	1.7	33
83	ImmobilizedCoffea arabica cell culture using a bubble-column reactor with controlled light intensity. Biotechnology and Bioengineering, 1993, 42, 494-502.	1.7	21
84	Nonisotropic Scattering Model for Estimation of Light Absorption Rates in a Suspension Culture of Coffea arabica Cells. Biotechnology Progress, 1993, 9, 86-92.	1.3	15
85	Influence of light irradiation rates and irradiation modes on caffeine production and cell growth in suspension culture of Coffea arabica cells.. Journal of Chemical Engineering of Japan, 1991, 24, 783-788.	0.3	10